

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

## (i) APPLICANT:

- (A) NAME: APPLIED RESEARCH SYSTEMS ARS HOLDING N.V.
- (B) STREET: 14 JOHN B. GROSIRAWEG
- (C) CITY: CURACAO
- (E) COUNTRY: NETHERLANDS ANTILLES
- (F) POSTAL CODE (ZIP): NONE
- (G) TELEPHONE: 639300
- (H) TELEFAX: 614129

(ii) TITLE OF INVENTION: INTRACELLULAR MODULATORS OF APOPTOTIC  
CELL  
DEATH PATHWAYS

(iii) NUMBER OF SEQUENCES: 6

## (iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

## (2) INFORMATION FOR SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1972 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 206..616

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CTGGCTGCTG TGGAGTTTGT GACATACTAG GTGACACCCT TGGAGTCACT TCTCTTCAAC  
60

TCCAGCTTAG AAGTGCCTGC CTGGCTCAGG GTCTGCACTG CAGCCTACTC CTTGCTTCAG  
120

GGCCTGACTG CAACGCCAAA GCCTATCCTA TAGCGGCAGC GCCAGCAGCC ACTCAAACCA  
180

GCCACAGCTC CCCGGCAACC GAACC ATG AAC ACC GAA ATG TAT CAG ACC CCC  
232

Met Asn Thr Glu Met Tyr Gln Thr Pro  
1 5

ATG GAG GTG GCG GTC TAT CAG CTG CAC AAT TTC TCC ACC TCC TTC TTT  
280

Met Glu Val Ala Val Tyr Gln Leu His Asn Phe Ser Thr Ser Phe Phe  
10 15 20 25

TCT TCT CTG CTT GGA GGG GAT GTG GTT TCC GTT AAA CTG GAT AAC AGT  
328

Ser Ser Leu Leu Gly Gly Asp Val Val Ser Val Lys Leu Asp Asn Ser  
30 35 40

GCC TCC GGA GCC AGT GTG GTG GCC CTA GAC AAC AAG ATT GAG CAG GCC  
376

Ala Ser Gly Ala Ser Val Val Ala Leu Asp Asn Lys Ile Glu Gln Ala  
45 50 55

ATG GAC CTC GTG AAG AAC CAC CTG ATG TAC GCT GTG AGA GAG GAG GTG  
424

Met Asp Leu Val Lys Asn His Leu Met Tyr Ala Val Arg Glu Glu Val  
60 65 70

GAG GTC CTA AAG GAG CAG ATT CGT GAG CTG CTT GAG AAG AAC TCC CAG  
472

Glu Val Leu Lys Glu Gln Ile Arg Glu Leu Leu Glu Lys Asn Ser Gln  
75 80 85

CTG GAG CGC GAG AAC ACC CTC CTG AAG ACG CTG GCA AGC CCC GAG CAA  
520

Leu Glu Arg Glu Asn Thr Leu Leu Lys Thr Leu Ala Ser Pro Glu Gln  
90 95 100 105

CTG GAA AAG TTC CAG TCC CGG CTG AGC CCT GAA GAG CCA GCA CCT GAA  
568

Leu Glu Lys Phe Gln Ser Arg Leu Ser Pro Glu Glu Pro Ala Pro Glu  
110 115 120

GCC CCA GAA ACC CCG GAA ACC CCG GAA GCC CCT GGT GGT TCT GCG GTG  
616

Ala Pro Glu Thr Pro Glu Thr Pro Glu Ala Pro Gly Gly Ser Ala Val  
125 130 135

TAAGTGGCTC TGTCCTTAGG GTGGGCAGAG CCACATCTTG TTCTACCTAG TTCTTTCCAG  
676

TTTGTTTTTG GCTCCCCAAG GGTCACTCTCA TGTGGAGAAC TTTACACCTA ACATAGCTGG  
736

TGCCAAGAGA TGTCCAAGG ACATGCCCAT CTGGGTCCAC TCCAGTGACA GACCCCTGAC  
796

AAAGAGCAGG TCTCTGGAGA CTAAGTTGCA TGGGGCCTAG TAACACCAAG CCAGTGAGCC  
856

TGTCGTGTCA CCGGGCCCTG GGGGCTCCCA GGGCTGGGCA ACTTAGTTAC AGCTGACCAA  
916

09403054.021100

GGAGAAAGTA GTTTTGAGAT GTGATGCCAG TGTGCTCCAG AAAGTGTAAG GGGTCTGTTT  
976

TTCATTTCCA TGGACATCTT CCACAGCTTC ACCTGACAAT GACTGTTCCCT ATGAAGAAGC  
1036

CACTTGTGTT CTAAGCAGAA GCAACCTCTC TCTTCTTCCT CTGTCTTTTC CAGGCAGGGG  
1096

CAGAGATGGG AGAGATTGAG CCAAATGAGC CTTCTGTTGG TTAATACTGT ATAATGCATG  
1156

GCTTTGTGCA CAGCCCAGTG TGGGGTTACA GCTTTGGGAT GACTGCTTAT AAAGTTCTGT  
1216

TTGGTTAGTA TTGGCATCGT TTTTCTATAT AGCCATAATG CGTATATATA CCCATAGGGC  
1276

TAGATCTATA TCTTAGGGTA GTGATGTATA CATATACACA TACACCTACA TGTTGAAGGG  
1336

CCTAACCAGC TTTGGGAGTA CTGACTGGTC TCTTATCTCT TAAAGCTAAG TTTTGGACTG  
1396

TGCTAATTTA CCAAATTGAT CCAGTTTGTC CTTTAGATTA AATAAGACTC GATATGAGGG  
1456

AGGGAGGGGA AGACCAGCCT CACAATGCGG CCACAGATGC CTTGCTGCTG CAGTCCTCCC  
1516

TGATCTGTCC ACTGAAGACA TGAAGTCCTC TTTTGAATGC CAAACCCACC ATTCATTGGT  
1576

GCTGACTACA TAGAATGGGG TTGAGAGAAG ATCAGTTTGG ACTTCACATT TTTGTTTTAA  
1636

GTTTGTAGTT GTTTTTTTTT GGTTTTGTTT GTTTGTTTGT TTGTTTGTTT TTGTTTTTTG  
1696

TTTTTCTTTT TTAAGTTCTT GTGGGGAAAC TTTGGGGTTA ATCAAAGGAT GTAGTCCTGT  
1756

GGTAGACCAG AGGAGTAACT AGTTTGTATC CTTTGGGGTG TGGAAAATGT ACCCAGGAAG  
1816

CTTGTGTAAG GAGGTTCTGT GACAGTGAAC ACTTCCACT TTCTGACACC TCATCCTGCT  
1876

GTACGACTCC AGGATTGGA TTTGGATTTT TCAAATGTAG CTTGAAATTT CAATAAACTT  
1936

TGCTCCTTTT TCTAAAAATA AAAAAAAAAA AAAAAA  
1972

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Asn Thr Glu Met Tyr Gln Thr Pro Met Glu Val Ala Val Tyr Gln  
1 5 10 15  
Leu His Asn Phe Ser Thr Ser Phe Phe Ser Ser Leu Leu Gly Gly Asp  
20 25 30  
Val Val Ser Val Lys Leu Asp Asn Ser Ala Ser Gly Ala Ser Val Val  
35 40 45  
Ala Leu Asp Asn Lys Ile Glu Gln Ala Met Asp Leu Val Lys Asn His  
50 55 60  
Leu Met Tyr Ala Val Arg Glu Glu Val Glu Val Leu Lys Glu Gln Ile  
65 70 75 80  
Arg Glu Leu Leu Glu Lys Asn Ser Gln Leu Glu Arg Glu Asn Thr Leu  
85 90 95  
Leu Lys Thr Leu Ala Ser Pro Glu Gln Leu Glu Lys Phe Gln Ser Arg  
100 105 110  
Leu Ser Pro Glu Glu Pro Ala Pro Glu Ala Pro Glu Thr Pro Glu Thr  
115 120 125  
Pro Glu Ala Pro Gly Gly Ser Ala Val  
130 135

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1..20  
(D) OTHER INFORMATION: /note= "PCR forward primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CCATCTGGGT CCACTCCAGT  
20

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "PCR reverse primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

AGGACAGTGG GAGTGGCACC  
20

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1946 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 241..642

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

AATTCGGGGG CCGTGGAGTT TGTGACATAC GAGGTGACAC CCCTCGAGTC ACTTCCCTTC  
60

AACTCCAGCT GGAGCGCCTG CTTGGCTTTG GGTTCGTTCT GCAGCCTTCG CCCCCTCCTC  
120

AGCCTCAGGG CCGGACTCCA GCGCAGAGCC CAGCCCAGCG CAGCCTGCCA GCAGCCACCC  
180

AGCCGCCCCAG CCGCCCAGCC CCGCACGAAA CCCGGCCAGA GCTTCCTAGC AGCCCGAGCC  
240

ATG AAC ACC GAA ATG TAT CAG ACC CCC ATG GAG GTG GCG GTC TAC CAG  
288  
Met Asn Thr Glu Met Tyr Gln Thr Pro Met Glu Val Ala Val Tyr Gln  
5 10 15

CTG CAC AAT TTC TCC ATC TCC TTC TTC TCT TCT CTG CTT GGA GGG GAT  
336  
Leu His Asn Phe Ser Ile Ser Phe Phe Ser Ser Leu Leu Gly Gly Asp  
20 25 30

GTG GTT TCC GTT AAG CTG GAC AAC AGT GCC TCC GGA GCC AGC GTG GTG  
384  
Val Val Ser Val Lys Leu Asp Asn Ser Ala Ser Gly Ala Ser Val Val  
35 40 45

GCC ATA GAC AAC AAG ATC GAA CAG GCC ATG GAT CTG GTG AAG AAT CAT  
432  
Ala Ile Asp Asn Lys Ile Glu Gln Ala Met Asp Leu Val Lys Asn His  
50 55 60

CTG ATG TAT GCT GTG AGA GAG GAG GTG GAG ATC CTG AAG GAG CAG ATC  
480  
Leu Met Tyr Ala Val Arg Glu Glu Val Glu Ile Leu Lys Glu Gln Ile  
65 70 75 80

CGA GAG CTG GTG GAG AAG AAC TCC CAG CTA GAG CGT GAG AAC ACC CTG  
528  
Arg Glu Leu Val Glu Lys Asn Ser Gln Leu Glu Arg Glu Asn Thr Leu  
85 90 95

TTG AAG ACC CTG GCA AGC CCA GAG CAG CTG GAG AAG TTC CAG TCC TGT  
576  
Leu Lys Thr Leu Ala Ser Pro Glu Gln Leu Glu Lys Phe Gln Ser Cys  
100 105 110

CTG AGC CCT GAA GAG CCA GCT CCC GAA TCC CCA CAA GTG CCC GAG GCC  
624  
Leu Ser Pro Glu Glu Pro Ala Pro Glu Ser Pro Gln Val Pro Glu Ala  
115 120 125

CCT GGT GGT TCT GCG GTG TAAGTGGCTC TGTCCTCAGG GTGGGCAGAG  
672  
Pro Gly Gly Ser Ala Val  
130

CCACTAAACT TGTTTTACCT AGTTCTTTCC AGTTTGTTTT TGGCTCCCCA AGCATCATCT  
732

CACGAGGAGA ACTTTACACC TAGCACAGCT GGTGCCAAGA GATGTCCTAA GGACATGGCC  
792

ACCTGGGTCC ACTCCAGCGA CAGACCCCTG ACAAGAGCAG GTCTCTGGAG GCTGAGTTGC  
852

ATGGGGCCTA GTAACACCAA GCCAGTGAGC CTCTAATGCT ACTGCGCCCT GGGGGCTCCC  
912

AGGGCCTGGG CAACTTAGCT GCAACTGGCA AAGGAGAAGG GTAGTTTGAG GTGTGACACC  
972

004403861 024400

AGTTTGCTCC AGAAAGTTTA AGGGGTCTGT TTCTCATCTC CATGGACATC TTCAACAGCT  
1032

TCACCTGACA ACGACTGTTT CTATGAAGAA GCCACTTGTG TTTTAAGCAG AGGCAACCTC  
1092

TCTCTTCTCC TCTGTTTCGT GAAGGCAGGG GACACAGATG GGAGAGATTG AGCCAAGTCA  
1152

GCCTTCTGTT GGTAAATATG GTATAATGCA TGGCTTTGTG CACAGCCCAG TGTGGGATTA  
1212

CAGCTTTGGG ATGACCGCTT ACAAAGTTCT GTTTGGTTAG TATTGGCATA GTTTTTCTAT  
1272

ATAGCCATAA ATGCGTATAT ATACCCATAG GGCTAGATCT GTATCTTAGT GTAGCGATGT  
1332

ATACATATAC ACATCCACCT ACATGTTGAA GGGCCTAACC AGCCTTGGA GTATTGACTG  
1392

GTCCCTTACC TCTTATGGCT AAGTCTTTGA CTGTGTTTAT TTACCAAGTT GACCCAGTTT  
1452

GTCTTTTAGG TTAAGTAAGA ACTCGAGAGT AAAGGCAAGG AGGGGGGCCA GCCTCTGAAT  
1512

GCGGCCACGG ATGCCTTGCT GCTGCAACCC TTTCCCCAGC TGTCCACTGA AACGTGAAGT  
1572

CCTGTTTTGA ATGCCAAACC CACCATTAC TGGTGCTGAC TACATAGAAT GGGTTGAGAG  
1632

AAGATCAGTT TGGGCTTCAC AGTGTCATTT GAAAAAGCGT TTTTGTTTTG TTTTGAATTA  
1692

TTGTGGAAAA CTTTCAAGTG AACAGAAGGA TGGTGTCCTA CTGTGGATGA GGGATGAACA  
1752

AGGGGATGGC TTTGATCCAA TGGAGCCTGG GAGGTGTGCC CAGAAAGCTT GTCTGTAGCG  
1812

GGTTTTGTGA GAGTGAACAC TTTCCACTTT TTGACACCTT ATCCTGATGT ATGGTTCCAG  
1872

GATTTGGATT TTGATTTTCC AAATGTAGCT TGAAATTTCATAAACTTTG CTCTGTTTTT  
1932

CTAAAAAATA AAAA  
1946

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 134 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Asn Thr Glu Met Tyr Gln Thr Pro Met Glu Val Ala Val Tyr Gln  
1 5 10 15  
Leu His Asn Phe Ser Ile Ser Phe Phe Ser Ser Leu Leu Gly Gly Asp  
20 25 30  
Val Val Ser Val Lys Leu Asp Asn Ser Ala Ser Gly Ala Ser Val Val  
35 40 45  
Ala Ile Asp Asn Lys Ile Glu Gln Ala Met Asp Leu Val Lys Asn His  
50 55 60  
Leu Met Tyr Ala Val Arg Glu Glu Val Glu Ile Leu Lys Glu Gln Ile  
65 70 75 80  
Arg Glu Leu Val Glu Lys Asn Ser Gln Leu Glu Arg Glu Asn Thr Leu  
85 90 95  
Leu Lys Thr Leu Ala Ser Pro Glu Gln Leu Glu Lys Phe Gln Ser Cys  
100 105 110  
Leu Ser Pro Glu Glu Pro Ala Pro Glu Ser Pro Gln Val Pro Glu Ala  
115 120 125  
Pro Gly Gly Ser Ala Val  
130

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